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OM protein - protein search, using sw model

Run on:
August 21, 2001, 12:06:13; Search time 16.04 Seconds
(without alignments)
1491.198 Million cell updates/sec

Title:
Sequence:
1641
Sequence:
1 MATCIDTCRTCNTQDDDSRF......IPCLTMDQTSYLTEWSDYVI 314

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters:
219241
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

RESULT S71181

N

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	ω H	30
164.5	171	175	175	177.5	179	207	217	217	265	287	312	338.5	359	365	369.5
10.0	10.4	10.7	10.7	10.8	10.9	12.6	13.2	13.2	16.1	17.5	19.0	20.6	21.9	22.2	22.5
190	201	240	236	143	256	184	162	162	231	319	171	220	171	171	269
ν	Ν	N	Ν	Ν	N	N	N	N	N	Ν	2	2	N	Н	<u>ш</u>
S07000	н85806	E83983	H72245	G82264	A86660	C82264	B85832	A64972	H83381	S55322	D84302	G72349	B71845	B64671	D43706
nodulation protein	hypothetical prote	tetrahydrodipicoli	2,3,4,5-tetrahydro	serine acetyltrans	acetyltransferase	serine acetyltrans	probable transfera	probable acetyl tr	probable acetyltra	srpH protein - Syn	serine acetyltrans	serine acetyltrans	o-serine acetyltra	serine O-acetyltra	serine O-acetyltra

ALIGNMENTS

Qy 301 DQTSYLTEWSDYVI 314	Qy 241 IGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKENPRKHDKIPCLTM	Qy 181 VDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQSGDRHPKIGDGVL 	Qy 121 KQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLMKQNRKIVALLIQNRVSESFA 	Qy 61 KQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELFISVLEESPEIIEST	Qy 1 MATCIDTCRTGNTQDDDSRFCCIKNFFRPGFSVNRKIHHTQIEDDDDVWIKMLEEAKSDV 	ngth 314 dels	RESULT 1 S67482 Serine O-acetyltransferase (EC 2.3.1.30), cytosolic - Arabidopsis thaliana N;Alternate names: serine acetyltransferase C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-2000 C;Accession: S67482; S52150 R;Ruffet, M.L.; Lebrun, M.; Droux, M.; Douce, R. Eur. J. Biochem. 227, 500-509, 1995 A;Title: Subcellular distribution of serine acetyltransferase from Pisum sa A;Reference number: S67482; MUID:95154333 A;Accession: S67482 A;Molecule type: DNA A;Residues: 1-314 <ruf> A;Cross-references: EMBL:234888; NID:9608676; PIDN:CAA84371.1; PID:9608677 A;Cross-references: EMBL:234888; NID:9608676; PIDN:CAA84371.1; PID:9608677 A;Note: the authors translated the codon ACC for residue 158 as Ile and ACA C;Superfamily: serine acetyltransferase; serine acetyltransferase homology C;Keywords: acyltransferase; coenzyme A; cysteine biosynthesis F;123-283/Domain: serine acetyltransferase homology <sat></sat></ruf>
	PRKHDKIPCLTM 300 RKHDKIPCLTM 300	3DRHPKIGDGVL 240 3DRHPKIGDGVL 240	LLIQNRVSESFA 180 LIQNRVSESFA 180	/LEESPEIIEST 120 /LEESPEIIEST 120	VIKMLEEAKSDV 60 VIKMLEEAKSDV 60	jth 314; els 0; Gaps 0;	- Arabidopsis thaliana text_change 05-May-2000 cansferase from Pisum sativum and sativum and pisum sativum and sativum sativum and sativum sativum and sativum sativum and sativum s

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A; Molecule type: mRNA
A; Residues: 1-391 <ROB>
A; Cross-references: EMBL:U22
A; Cross-references: EMBL:U22
R; Hell, R.
submitted to the EMBL Data L
A; Reference number: S71906
A; Accession: S71906
A; Molecule type: mRNA
A; Residues: 80-391 <HEL>
A; Cross-references: EMBL:X82
C; Genetics:
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A; Genome: nuclear
C; Superfamily: serine acetyltransferase; serine acetyltransfera C; Keywords: acyltransferase; chloroplast; coenzyme A; cysteine F; 123-283/Domain: serine acetyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                     R;Roberts, M.A.; Wray, J.L.
Plant Mol. Biol. 30, 1041-1049, 1996
A;Title: Cloning and characterisation of an A;Reference number: S69192; MUID:96270381
A;Accession: S69192
A; Genome:
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C;Date: 05-Dec-196 #sequence_revision 27-Feb-1997 #text_change 05-May-2000
C;Accession: S69192; S71906
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A; Residues: 1-314 < MUR>
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A; Accession: S71181
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Species: Arabidopsis thaliana (mouse-ear cress)
Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change
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                                                              EMBL: x82888; NID: g897677; PIDN: CAA58061.1; PID: g897678
                                                                                                                                                                                                                                 EMBL: U22964; NID: g1184047;
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86
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A;Gene: satA
C;Superfamily: serine acetyltransferase; serine acetyltransferase homology C;Keywords: acyltransferase; coenzyme A; cysteine biosynthesis F;113-272/Domain: serine acetyltransferase homology <SAT>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_ch
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A; Residues: 1-303 <BO
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Lett. 358, 43-47, 1995
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                                                     ASIVSQRSYEAALANTLSVKLSNLNLPSNTLFDLFSGVLQGNPDIVESVKLDLLAVKERD
                                                                                                                                 NYFRYPDRSSFNGTQTKTLHTRPLLEDLDRDAEVDDVWAKIREEAKSDIAKEPIVSAYYH
                                                                                                                                                                     NFFR-PGFS----VNRKIHHTQ--IED-----DDDVWIKMLEEAKSDVKQEPILSNYYY
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                                                                                           ASITSHRSLESALAHILSVKLSNLNLPSNTLFELFISVLEESPEIIESTKQDLIAVKERD
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73.0%;
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Pred. No. 2
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Pred. No. 2.9e-93;
                                                                                                                                                                                                               Mismatches
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2.8e-84;
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PACISYVHCFLHFKGFLACQAHRIAHELWTQDRKILALLIQNRVSEAFAVDFHPGAKIGT

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A; Experimental source: leaf C; Function:
C; Function:
A; Description: catalyzes conversion of L-serine to O-acetyl serine A; Description: catalyzes conversion of L-serine to O-acetyl serine A; Pathway: cysteine biosynthesis
C; Superfamily: serine acetyltransferase; serine acetyltransferase h C; Keywords: acyltransferase; coenzyme A; cysteine biosynthesis F; 156-316/Domain: serine acetyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Spinacia oleracea (spinach)
C;Date: 11-Jun-1999 #sequence_revision
C;Accession: T09110
R;Saito, K; Takagi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
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A; Residues: 1-347 <SAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, Oc A; Description: A cDNA encoding serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serine O-acetyltransferase (EC 2.3.1.30) - spinach N; Alternate names: serine acetyltransferase
C;Species: Citrullus lanatus (watermelon)
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-19
C;Accession: A57478
R;Saito, K.; Yokoyama, H.; Noji, M.; Murakoshi,
J. Biol. Chem. 270, 16321-16326, 1995
A;Title: Molecular cloning and characterization
A;Reference number: A57478; MUID:95332343
                                                                                                                 serine O-acetyltransferase (EC 2.3.1.30) - watermelon C; Species: Citrullus lanatus (watermelon)
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A57478
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                                                                                                                                                                                                                                                                                KDVPARTTAVGNPARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
                                                                                                                                                                                                                                                                                                                                                          AVVGDNVSILHGVTLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVV
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                                                                                                                                                                                                                                                                                                                       ATTGDNCSTLHHVTLGGTGKAGGDRHPKVGDGVLTGAGATTLGNVRTGDGAKTGAGSVVL
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Pred. No. 2.
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A;Accession: A57478;
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Status: properties: CSB:D49535; NID:g1060871; PIDN:BAA08479.1; PID:g1841312
C;Superfamily: serine acetyltransferase; serine acetyltransferase homology
C;Keywords: acyltransferase; coenzyme A
F;103-263/Domain: serine acetyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: $71207

A; Accession: $71207

A; Accession: $71207

A; Molecule type; mRNA

A; Residues: 1-312 <HOW>
A; Residues: 1-312 <HOW>
A; Cross references: EMBL: U30298; NID: 9905390; PIDN: AAC49655.1; PID: 9905391
C; Superfamily: serine acetyltransferase; serine acetyltransferase homology
C; Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
F; 120-280/Domain: serine acetyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      serine O-acetyltransferase (EC 2.3.1.30) Sat-52 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May C;Accession: S71207
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                                                                                                                                                                                                                                                                                                                           VWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELFI 107
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CGDRHPKIGDGCLIGAGATILGNVKIGAGAKVGAGSVVLIDVPCRGTAVGNPARLVGGKE
                                            SGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKE 287
                                                                                          ALALHSRISDVFAVDIHPAAKIGKGILLDHATGVVVGETAVIGNNVSILHHVTLGGTGKA
                                                                                                                     ALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQ
                                                                                                                                                                                          NTFSSDPSLRNATVADLRAARVRDPACISFSHCLLNYKGFLATQAHRVSHKLWTQSRKPL
                                                                                                                                                                                                                                   SVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIV
                                                                                                                                                                                                                                                                                    LWTQIKAEARRDAEAEPALASYLYSTILSHSSLERSISFHLGNKLCSSTLLSTLLYDLFL
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                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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59.7%;
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Pred. No. 1.1e-64;
                                                                                                                                                                                                                                                                                                                                                                               Score 849.5; DB (
Pred. No. 4.9e-63;
5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58
A;Reference number: A81000; MUID:20175755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; I
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougher
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza,
Science 287, 1809-1815, 2000
                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-272 <TET>
                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A81000; A; Accession: C81184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable serine O-acetyltransferase (EC 2.3.1.30) NMA0742 [imported] - Neis C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001 C;Accession: C81184; H81917
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A;Map position: 2
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A;Accession: F84554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 AAGSLVLKDVPSHSVVAGNPAKLIRVME-----EQDPSLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 GSGSVVVKDVPARTTAVGNPARLIGGKENPRKHDKIPCLTM 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVVIGETAVVGDNVSILHGVTLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CFLGFKGFLACQAHRIAHTLWKQNRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHAT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEQALGFVLANRLQNPTLLATQLLDIFYGVMMHDKGIQSSIRHDLQAFKDRDPACLSYSS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FESGFEVYAKGTHKSEFDSNLLDPRSDPIWDAIREEAK--LEKEPILSSFLYAGILAHDC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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50.2%;
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Pred. No. 1.6e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rappuoli, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dougherty,
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                                                             Morel
A;Residues: 1-273 <PLU>
A;Residues: 1-273 <PLU>
A;Cross-references: EMBL:U00039; NID:g466582; PIDN:AAB18584.1; PID:g466745
A;Cross-references: EMBL:U00039; PID:g46674582; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M15745; NID:g145675; PIDN:AAA23648.1; PID:g145676 R;Tei, H.; Murata, K.; Kimura, A. Biochem. Biophys. Res. Commun. 167, 948-955, 1990 A;Title: Structure and expression of CYSX, the second gene in the Escher A;Reference number: A34563; MUID:90211342 A;Accession: A34563
                                                                                                                                                                                                                                                                                                R; Plunkett, G. submitted to the EMBL Data A; Reference number: S47666 A; Accession: S47828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M34333; NID:g145693; PIDN:AAA23659.1; PID:g145694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-273 <TEI>
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A; Residues: 1-273 <DEN>
                                                                                                                                                                                                                                            A; Molecule type: DNA
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Library, March

Riley,

the Escherichia coli K-

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C;Species: Escherichia coli
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
C;Accession: A27896; A34563; S47828; A65161
A; Title: L-Cysteine biosynthesis in Escherichia coli: nucleotide A; Reference number: A27896; MUID:88009872
                                                        R;Denk, D.; Bock, A.
J. Gen. Microbiol. 133, 515-525, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: cysE; NMB0560; NMA0742
C;Superfamily: serine acetyltransferase; serine acetyltransferase homology
C;Keywords: acyltransferase; coenzyme A
F;88-248/Domain: serine acetyltransferase homology <SAT>
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                                                                                                                                                                                                 serine O-acetyltransferase (EC 2.3.1.30) - Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: serogroup C; Genetics:
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A; Residues: 1-272 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                   287 ENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 VALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 QSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 QQALGSDTQIGKCVEADLKAIYERDPACDEYSLPLLYFKGFHAIQAHRINHRLYLDGRKT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGGDRHPKIGDGVMIGANASILGNIRIGSNAKIGAGSVVVSDVPPSITVVGVPAKPVA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLWHTIREETAAAVSAEPMLASFLHQTVLRHESLGSVLAYHLSSKLGSPIMDVRALFEIY
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serine O-acetyltransferase (EC 2.3.1.30) - Salmonella typhimurium C;Species: Salmonella typhimurium C;Species: Salmonella typhimurium C;Date: 25-Feb:1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000 C;Accession: S29568
R;Sivaprasad, A.V.; Kuczek, E.S.; Bawden, C.S.; Rogers, G.E. submitted to the EMBL Data Library, May 1991
A;Description: A novel biosynthetic pathway for mammalian cells by stable integration A;Reference number: S29567
A;Reference number: S29567
A;Accession: S29568
A;Molecule type: DNA
A;Residues: 1-273 <SIV>
A;Cress-references: EMBL:X59594; NID:947659; PIDN:CAA42163.1; PID:947660
C;Superfamily: serine acetyltransferase; serine acetyltransferase; Serine acetyltransferase homology <SAT>
F;84-244/Domain: serine acetyltransferase homology <SAT>
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A;Station: A65161
A;Station: A65161
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                                                                  FELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGKPDS----DK-PSMDMDQ 258
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      REVVEEAYAADPEMTASAACDIQAVRTRDPAVDKYSTPLLYLKGFHALQAYRIGHWLWNK 123
                                                                                                                                  EELEIVWKNIKAEARALADCEPMLASFYHATLLKHENLGSALSYMLANKLASPIMPAIAI 63
                                                                                                                                                                                              EDDDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGGKENPRKHDKIPCLTMDQ 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARL 282
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                                                                                                                                                                                                                                                                                            Score 648.5; DB Pred. No. 2e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                            R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sell l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                   serine acetyltransferase VC2649 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio A; Reference number: A82035; MUID: 20406833
                                                                                                                                                                                                                                                                                                                       RESULT 13
G82049
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\begin{array}{lll} A; Gene: \ cysE \\ C; Superfamily: \ serine \ acetyltransferase; \ serine \ acetyltransferase \ homology \end{array}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serine acetyltransferase [imported] - Escherichia coli (strain 0157:H7) C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C;Accession: F86036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           k;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasr
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta,
Nature 409, 529-533, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005174; NID:g12518357; PIDN:AAG58754.1; A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-273 <STO>
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Best Local
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                             IGGKENPRKHDKIPCLTMDQ 302
                                                                                                GTGKSGGDRHPKIREGVMIGAGAKILGNIEVGRGAKIGAGSVVLQPVPPHTTAAGVPARI
                                                                                                                                                                                                      GRRALAIFLQNQVSVTFQVDIHPAAKIGRGIMLDHATGIVVGETAVIENDVSILQSVTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDDDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRRALAIFLQNQVSVSFQVDIHPAAKIGRGIMLDHATGIVVGETAVIEDDVSILQSVTLG
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VGKPDS----DK-PSMDMDQ 258
                                                                                                                                              GTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARL
                                                                                                                                                                                                                                                       NRKIVALLIONRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLG
                                                                                                                                                                                                                                                                                                          REVVEEAYAADPEMIASAACDIQAVRTRDPAVDKYSTPLLYLKGFHALQAYRIGHWLWNQ
                                                                                                                                                                                                                                                                                                                                                             FELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQ 162
                                                                                                                                                                                                                                                                                                                                                                                                             EELEIVWNNIKAEARTLADCEPMLASFYHATLLKHENLGSALSYMLANKLSSPIMPAIAI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGGKENPRKHDKIPCLTMDQ 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.5%; Score 648.5; DB 50.8%; Pred. No. 2e-46; tive 51; Mismatches
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imalanta, E.;
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K.; Apoda
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cholerae

Sellers

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submitted to the EMBL Data Library, October 1997

A:Reference number: Z16500

A:Accession: T08867

A:Status: translated from GB/EMBL/DDBJ

A:Residues: 1-308 <WAT>
A:Coss references: EMBL:AF024504; NID:92435510; PID:92435513; GSPDB:GN00062; ATSP:A_TMCA:Experimental source: cultivar Columbia; BAC clone TM017A05

C:Genetics:
A:Genetics:
A:Gene: ATSP:A_TM017A05.1

A:Map position: 4
A:Introns: 47/3; 113/3; 139/2; 181/1; 212/3; 273/2; 298/1
A:Introns: 47/3; 113/3; 139/2; 181/1; 212/3; 273/2; 298/1
C:Superfamily: serine acetyltransferase; serine acetyltransferase homology
C:Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
F:111-283/Domain: serine acetyltransferase homology <SAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: VC2649
A;Map position: 1
C;Superfamily: serine
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-273 <HEI>
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                                                                                                            FRPGFSVNRK-IHHTQIEDD------DDVWIKMLEEAKSDVKQEPILSNYYYASITSHRS 79
LEQALGFYLANRLQNPTLLATQLLDIFYGYMMHDKGIQSSIRHDLQAFKDRDPACLSYSS 127
                      LESALAHILSVKLSNLNLPSNTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVH 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LWRQGRKALATYFQNQISVACQVDIHPAARIGRGIMLDHATGIVIGETAVVEDDVSILQD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTQIEDDDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLP 98
                                                                                     FESGFEVYAKGTHKSEFDSNLLDPRSDPIWDAIREEAKLEAEKEPILSSFLYAGILAHDC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTLGGTGKECGDRHPKIREGVMIGAGAKILGNIEVGEGAKIGSGSVVLQAVPPHTTVAGV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LWKQNRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMAVREVIEEAFAADPSISEAAACDICATVNRDPAVSMYSMPLLYLKGYHALQGYRVANW 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTK-----VWQTIVAEAREQAEQEPMLASFYHATIIKHDSLKAALSYILANRLNTASMP
                                                                                                                                                                           138;
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45.2%;
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Pred. No. 2.4
                                                                                                                                                                                             Score 643; DB 2;
Pred. No. 6.8e-46;
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ches 71;
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R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Hacmophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Way-2000
C;Accession: G64080
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A; Residues: 1-267 <TIGR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serine O-acetyltransferase (EC 2.3.1.30) - Haemophilus influenzae (strain Rd KW20)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 CF-----LGFKGFLACQAHRIAHTLWKQNRKIVALLIQNRVSESFAVDIHPG
                                                                                                                                                                                                                                                            167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 ARIGEGILLDHGTGVVIGETAVIGNGVSILHFSLSQGVTLGGTGKETGDRHPKIGEGALL
                                                287 ENPRKHDKI -- PCLTMDQ 302
                                                                                                                                                                                                                                                                                                                   64
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                                                                                                                                                                                                                                                            VALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGK 226
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----SQDKAAKPAFDMNQ
                                                                                                                                                        QSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGK 286
                                                                                                                                                                                                                                                                                                                EEAYQSNPSIIDCAACDIQAVRHRDPAVELWSTPLLYLKGFHAIQSYRITHYLWNQNRKS 123
                                                                                                                                                                                                                                                                                                                                                                 ISVLEESPEITESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKI 166
                                                                                                                                                                                                                                                                                                                                                                                                                       DVWQHIRQEAKELAENEPMLASFFHSTILKHQNLGGALSYLLANKLANPIMPAISLREII 63
                                                                                                       ESGDRHPKVREGVMIGAGAKILGNIEVGKYAKIGANSVVLNPVPEYATAAGVPARIV---
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4; Mismatches 70
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